

RAW SEQUENCE LISTING

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Application Serial Number: 10/510,034
Source: PCT
Date Processed by STIC: 04/11/2006

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RAW SEQUENCE LISTING

DATE: 04/11/2006

PATENT APPLICATION: US/10/510,034

TIME: 12:42:08

Input Set : A:\2005-10-03 3671-0110PUS1.ST25.txt

Output Set: N:\CRF4\04112006\J510034.raw

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3 <110> APPLICANT: PAN Shen Quan
5 <120> TITLE OF INVENTION: VISUALIZATION OF INTRODUCED DNA (VOID) IN TRANSIT BY IN SITU
6   HYBRIDIZATION
8 <130> FILE REFERENCE: 3671-0110PUS1
10 <140> CURRENT APPLICATION NUMBER: US 10/510,034
11 <141> CURRENT FILING DATE: 2004-10-01
13 <150> PRIOR APPLICATION NUMBER: US 60/368,524
14 <151> PRIOR FILING DATE: 2002-04-01
16 <160> NUMBER OF SEQ ID NOS: 11
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 887
22 <212> TYPE: PRT
23 <213> ORGANISM: Arabidopsis thaliana
25 <400> SEQUENCE: 1
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28 1          5          10          15
31 Ala Ala Ile Glu Gly Thr Lys Gln Ser Ile Val Met Ser Ile Arg Val
32          20          25          30
35 Ala Lys Ser Arg Gly Val Trp Gly Lys Ser Gly Lys Leu Gly Arg Gln
36          35          40          45
39 Met Ala Lys Pro Arg Val Leu Ala Leu Ser Val Lys Ser Lys Gly Pro
40          50          55          60
43 Arg Lys Lys Ala Phe Leu Arg Val Met Lys Tyr Ser Ser Gly Gly Val
44 65          70          75          80
47 Leu Glu Pro Ala Lys Met Tyr Lys Leu Lys His Leu Ser Lys Val Glu
48          85          90          95
51 Val Ile Thr Asn Asp Pro Ser Gly Cys Thr Phe Thr Leu Gly Phe Asp
52          100         105         110
55 Asn Leu Arg Ser Gln Ser Val Ala Pro Pro Gln Trp Thr Met Arg Asn
56          115         120         125
59 Thr Asp Asp Arg Asn Arg Leu Leu Val Cys Ile Leu Asn Ile Cys Lys
60          130         135         140
63 Asp Val Leu Gly Arg Leu Pro Lys Val Val Gly Ile Asp Ile Val Glu
64 145         150         155         160
67 Met Ala Leu Trp Ala Lys Asp Asn Thr Pro Val Val Thr Thr Gln Arg
68          165         170         175
71 Ser Thr Glu Asp Gly Glu Pro Val Ala Glu Ser Val Thr Glu Ser Asp
72          180         185         190
75 Leu Lys Val Thr Val Glu Lys Glu Leu Val Ser Gln Ala Glu Glu Glu
76          195         200         205
79 Asp Met Glu Ala Leu Leu Gly Thr Tyr Val Met Gly Ile Gly Glu Ala
80          210         215         220

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83 Glu Ala Phe Ser Glu Arg Leu Lys Arg Glu Leu Gln Ala Leu Glu Ala
84 225                230                235                240
87 Ala Asn Val His Ala Ile Leu Glu Ser Glu Pro Leu Val Asp Glu Val
88                245                250                255
91 Leu Asn Gly Leu Glu Ala Ala Thr Asn Ile Val Asp Asp Met Asp Glu
92                260                265                270
95 Trp Leu Gly Ile Phe Asn Ile Lys Leu Arg His Met Arg Glu Asp Ile
96                275                280                285
99 Glu Ser Ile Glu Thr Arg Asn Asn Lys Leu Glu Met Gln Ser Val Asn
100 290                295                300
103 Asn Lys Ala Leu Ile Glu Leu Asp Lys Val Ile Glu Arg Leu Arg
104 305                310                315                320
107 Val Pro Ser Glu Tyr Ala Ala Ser Leu Thr Gly Gly Ser Phe Asp Glu
108                325                330                335
111 Ala Asp Met Leu Gln Asn Ile Glu Ala Cys Glu Trp Leu Ala Lys Ala
112                340                345                350
115 Leu Arg Gly Leu Glu Val Pro Asn Leu Asp Pro Ile Tyr Ala Asn Met
116                355                360                365
119 Arg Ala Val Lys Glu Lys Arg Ala Glu Leu Glu Lys Leu Lys Ala Thr
120 370                375                380
123 Phe Val Arg Arg Ala Ser Glu Phe Leu Arg Asn Tyr Phe Ala Ser Leu
124 385                390                395                400
127 Val Asp Phe Met Val Ser Asp Lys Ser Tyr Phe Ser Gln Arg Gly Gln
128                405                410                415
131 Leu Lys Arg Pro Asp His Ala Asp Leu Arg Tyr Lys Cys Arg Thr Tyr
132                420                425                430
135 Ala Arg Leu Leu Gln His Leu Lys Gly Leu Asp Lys Asn Cys Leu Gly
136                435                440                445
139 Pro Leu Arg Lys Ala Tyr Cys Ser Ser Leu Asn Leu Leu Arg Arg
140                450                455                460
143 Glu Ala Arg Glu Phe Ala Asn Glu Leu Arg Ala Ser Thr Lys Val Ser
144 465                470                475                480
147 Arg Asn Pro Thr Val Trp Leu Glu Gly Ser Thr Gly Ser Ser Gln Asn
148                485                490                495
151 Ala Asn Thr Asp Thr Ser Ala Val Ser Asp Ala Tyr Ala Lys Met Leu
152                500                505                510
155 Thr Ile Phe Ile Pro Leu Leu Val Asp Glu Ser Ser Phe Phe Ala His
156                515                520                525
159 Phe Met Cys Phe Glu Val Pro Ala Leu Ala Pro Pro Gly Gly Ala Gly
160                530                535                540
163 Asn Asp Lys Lys Ser Gln Ser Asn Asn Asp Asp Gly Asn Asp Asp Asp
164 545                550                555                560
167 Asp Leu Gly Ile Met Asp Ile Asp Glu Thr Asp Lys Lys Pro Gly Lys
168                565                570                575
171 Asn Ser Pro Asp Leu Thr Ala Leu Asn Glu Ser Leu Gln Asp Leu Leu
172                580                585                590
175 Asp Gly Ile Gln Glu Asp Phe Tyr Ala Val Val Asp Trp Ala Tyr Lys
176                595                600                605
179 Ile Asp Pro Leu Arg Cys Ile Ser Met His Gly Ile Thr Glu Arg Tyr

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180      610      615      620
183 Leu Ser Gly Gln Lys Ala Asp Ala Ala Gly Phe Val Arg Leu Leu Leu
184 625      630      635      640
187 Gly Asp Leu Glu Ser Arg Val Ser Met Gln Phe Ser Arg Phe Val Asp
188      645      650      655
191 Glu Ala Cys His Gln Ile Glu Arg Asn Glu Arg Asn Val Arg Gln Met
192      660      665      670
195 Gly Val Leu Pro Tyr Ile Pro Arg Phe Ala Ala Leu Ala Thr Arg Met
196      675      680      685
199 Glu Gln Tyr Ile Gln Gly Gln Ser Arg Asp Leu Val Asp Gln Ala Tyr
200      690      695      700
203 Thr Lys Phe Val Ser Ile Met Phe Val Thr Leu Glu Lys Ile Ala Gln
204 705      710      715      720
207 Gln Asp Pro Lys Tyr Ala Asp Ile Leu Leu Glu Asn Tyr Ala Ala
208      725      730      735
211 Phe Gln Asn Ser Leu Tyr Asp Leu Ala Asn Val Val Pro Thr Leu Ala
212      740      745      750
215 Lys Phe Tyr His Gln Ala Ser Glu Ala Tyr Glu Gln Ala Cys Thr Arg
216      755      760      765
219 His Ile Ser Met Ile Ile Tyr Tyr Gln Phe Glu Arg Leu Phe Gln Phe
220      770      775      780
223 Ala Lys Lys Ile Glu Asp Phe Met Tyr Thr Ile Thr Pro Glu Glu Ile
224 785      790      795      800
227 Pro Phe Gln Leu Gly Leu Ser Lys Val Glu Leu Arg Lys Met Leu Lys
228      805      810      815
232 Ser Ser Leu Ser Gly Val Asp Lys Ser Ile Ala Ala Met Tyr Lys Lys
233      820      825      830
236 Leu Gln Lys Asn Leu Ala Ser Glu Glu Leu Leu Pro Ser Leu Trp Asp
237      835      840      845
240 Lys Cys Lys Lys Glu Phe Leu Asp Lys Tyr Glu Ser Phe Val Gln Leu
241      850      855      860
244 Val Ala Lys Val Tyr Pro Ser Glu Asn Val Pro Gly Val Thr Glu Met
245 865      870      875      880
248 Arg Gly Leu Leu Ala Ser Met
249      885
252 <210> SEQ ID NO: 2
253 <211> LENGTH: 15
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Synthetic GUS-1 primer
260 <400> SEQUENCE: 2
261 cgtcctgtag aaacc
264 <210> SEQ ID NO: 3
265 <211> LENGTH: 15
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Synthetic GUS-2 primer

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272 <400> SEQUENCE: 3
273 acgcacagtt catag 15
276 <210> SEQ ID NO: 4
277 <211> LENGTH: 15
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Synthetic BIN19-1 primer
284 <400> SEQUENCE: 4
285 ttgctcatgt taccg 15
289 <210> SEQ ID NO: 5
290 <211> LENGTH: 15
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Synthetic BIN19-2 primer
297 <400> SEQUENCE: 5
298 gcagttccgc aaata 15
301 <210> SEQ ID NO: 6
302 <211> LENGTH: 27
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Synthetic Oligo-105 primer
309 <400> SEQUENCE: 6
310 gaagaattcg aacttgacgc cgatacc 27
313 <210> SEQ ID NO: 7
314 <211> LENGTH: 24
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Synthetic Oligo-107 primer
321 <400> SEQUENCE: 7
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324 <210> SEQ ID NO: 8
325 <211> LENGTH: 894
326 <212> TYPE: PRT
327 <213> ORGANISM: Homo sapiens
329 <400> SEQUENCE: 8
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332 1 5 10 15
335 Asp Glu Arg Leu Leu Ser Ile Val Asn Val Cys Lys Ala Gly Lys Lys
336 20 25 30
339 Lys Lys Asn Cys Phe Leu Cys Ala Thr Val Thr Thr Glu Arg Pro Val
340 35 40 45
343 Gln Val Lys Val Val Lys Val Lys Lys Ser Asp Lys Gly Asp Phe Tyr
344 50 55 60
347 Lys Arg Gln Ile Ala Trp Ala Leu Arg Asp Leu Ala Val Val Asp Ala
348 65 70 75 80

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351 Lys Asp Ala Ile Lys Glu Asn Pro Glu Phe Asp Leu His Phe Glu Lys
352      85      90      95
355 Ile Tyr Lys Trp Val Ala Ser Ser Thr Ala Glu Lys Asn Ala Phe Ile
356      100     105     110
359 Ser Cys Ile Trp Lys Leu Asn Gln Arg Tyr Leu Arg Lys Lys Ile Asp
360      115     120     125
363 Phe Val Asn Val Ser Ser Gln Leu Leu Glu Glu Ser Val Pro Ser Gly
364      130     135     140
367 Glu Asn Gln Ser Val Thr Gly Gly Asp Glu Glu Val Val Asp Glu Tyr
368 145      150     155     160
371 Gln Glu Leu Asn Ala Arg Glu Glu Gln Asp Ile Glu Ile Met Met Glu
372      165     170     175
375 Gly Cys Glu Tyr Ala Ile Ser Asn Ala Glu Ala Phe Ala Glu Lys Leu
376      180     185     190
379 Ser Arg Glu Leu Gln Val Leu Asp Gly Ala Asn Ile Gln Ser Ile Met
380      195     200     205
383 Ala Ser Glu Lys Gln Val Asn Ile Leu Met Lys Leu Leu Asp Glu Ala
384      210     215     220
387 Leu Lys Glu Val Asp Gln Ile Glu Leu Lys Leu Ser Ser Tyr Glu Glu
388 225      230     235     240
391 Met Leu Gln Ser Val Lys Glu Gln Met Asp Gln Ile Ser Glu Ser Asn
392      245     250     255
395 His Leu Ile His Leu Ser Asn Thr Asn Asn Val Lys Leu Leu Ser Glu
396      260     265     270
399 Ile Glu Phe Leu Val Asn His Met Asp Leu Ala Lys Gly His Ile Lys
400      275     280     285
403 Ala Leu Gln Glu Gly Asp Leu Ala Ser Ser Arg Gly Ile Glu Ala Cys
404      290     295     300
407 Thr Asn Ala Ala Asp Ala Leu Leu Gln Cys Met Asn Val Ala Leu Arg
408 305      310     315     320
411 Pro Gly His Asp Leu Leu Leu Ala Val Lys Gln Gln Gln Gln Arg Phe
412      325     330     335
415 Ser Asp Leu Arg Glu Leu Phe Ala Arg Arg Leu Ala Ser His Leu Asn
416      340     345     350
419 Asn Val Phe Val Gln Gln Gly His Asp Gln Ser Ser Thr Leu Ala Gln
420      355     360     365
423 His Ser Val Glu Leu Thr Leu Pro Asn His His Pro Phe His Arg Asp
424      370     375     380
427 Leu Leu Arg Tyr Ala Lys Leu Met Glu Trp Leu Lys Ser Thr Asp Tyr
428 385      390     395     400
431 Gly Lys Tyr Glu Gly Leu Thr Lys Asn Tyr Met Asp Tyr Leu Ser Arg
432      405     410     415
435 Leu Tyr Glu Arg Glu Ile Lys Asp Phe Phe Glu Val Ala Lys Ile Lys
436      420     425     430
439 Met Thr Gly Thr Thr Lys Glu Ser Lys Lys Phe Ala Thr Leu Pro Arg
440      435     440     445
443 Lys Glu Ser Ala Val Lys Gln Glu Thr Glu Ser Leu His Gly Ser Ser
444      450     455     460
447 Gly Lys Leu Thr Gly Ser Thr Ser Ser Leu Asn Lys Leu Ser Val Gln

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VERIFICATION SUMMARY

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